

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: E. I. DU PONT DE NEMOURS AND  
COMPANY
- (ii) TITLE OF INVENTION: CHIMERIC GENES AND  
METHODS FOR INCREASING  
INCREASING THE LYSINE  
AND THREONINE CONTENT  
OF THE SEEDS OF PLANTS
- (iii) NUMBER OF SEQUENCES: 107
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: E. I. DU PONT DE NEMOURS  
AND COMPANY
  - (B) STREET: 1007 MARKET STREET
  - (C) CITY: WILMINGTON
  - (D) STATE: DELAWARE
  - (E) COUNTRY: U.S.A.
  - (F) ZIP: 19898
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: FLOPPY DISK
  - (B) COMPUTER: IBM PC COMPATIBLE
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: MICROSOFT WORD VERSION 2.0C
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: BARBARA C. SIEGELL
  - (B) REGISTRATION NUMBER: 30,684
  - (C) REFERENCE/DOCKET NUMBER: BB-1037-C
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 302-992-4931
  - (B) TELEFAX: 302-773-0164
  - (C) TELEX: 835420

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG GCT GAA ATT GTT GTC TCC AAA TTT GGC GGT ACC AGC GTA GCT GAT	48
Met Ala Glu Ile Val Val Ser Lys Phe Gly Gly Thr Ser Val Ala Asp	
1 5 10 15	
TTT GAC GCC ATG AAC CGC AGC GCT GAT ATT GTG CTT TCT GAT GCC AAC	96
Phe Asp Ala Met Asn Arg Ser Ala Asp Ile Val Leu Ser Asp Ala Asn	
20 25 30	
GTG CGT TTA GTT GTC CTC TCG GCT TCT GCT GGT ATC ACT AAT CTG CTG	144
Val Arg Leu Val Val Leu Ser Ala Ser Ala Gly Ile Thr Asn Leu Leu	
35 40 45	
GTC GCT TTA GCT GAA GGA CTG GAA CCT GGC GAG CGA TTC GAA AAA CTC	192
Val Ala Leu Ala Glu Gly Leu Glu Pro Gly Glu Arg Phe Glu Lys Leu	
50 55 60	
GAC GCT ATC CGC AAC ATC CAG TTT GCC ATT CTG GAA CGT CTG CGT TAC	240
Asp Ala Ile Arg Asn Ile Gln Phe Ala Ile Leu Glu Arg Leu Arg Tyr	
65 70 75 80	
CCG AAC GTT ATC CGT GAA GAG ATT GAA CGT CTG CTG GAG AAC ATT ACT	288
Pro Asn Val Ile Arg Glu Glu Ile Glu Arg Leu Leu Glu Asn Ile Thr	
85 90 95	
GTT CTG GCA GAA GCG GCG GCG CTG GCA ACG TCT CCG GCG CTG ACA GAT	336
Val Leu Ala Glu Ala Ala Ala Leu Ala Thr Ser Pro Ala Leu Thr Asp	
100 105 110	
GAG CTG GTC AGC CAC GGC GAG CTG ATG TCG ACC CTG CTG TTT GTT GAG	384
Glu Leu Val Ser His Gly Glu Leu Met Ser Thr Leu Leu Phe Val Glu	
115 120 125	
ATC CTG CGC GAA CGC GAT GTT CAG GCA CAG TGG TTT GAT GTA CGT AAA	432
Ile Leu Arg Glu Arg Asp Val Gln Ala Gln Trp Phe Asp Val Arg Lys	
130 135 140	
GTG ATG CGT ACC AAC GAC CGA TTT GGT CGT GCA GAG CCA GAT ATA GCC	480
Val Met Arg Thr Asn Asp Arg Phe Gly Arg Ala Glu Pro Asp Ile Ala	
145 150 155 160	
GCG CTG GCG GAA CTG GCC GCG CTG CAG CTG CTC CCA CGT CTC AAT GAA	528
Ala Leu Ala Glu Leu Ala Ala Leu Gln Leu Leu Pro Arg Leu Asn Glu	

165										170										175									
GGC	TTA	GTG	ATC	ACC	CAG	GGA	TTT	ATC	GGT	AGC	GAA	AAT	AAA	GGT	CGT	576													
Gly	Leu	Val	Ile	Thr	Gln	Gly	Phe	Ile	Gly	Ser	Glu	Asn	Lys	Gly	Arg														
180										185						190													
ACA	ACG	ACG	CTT	GGC	CGT	GGA	GGC	AGC	GAT	TAT	ACG	GCA	GCC	TTG	CTG	624													
Thr	Thr	Thr	Leu	Gly	Arg	Gly	Gly	Ser	Asp	Tyr	Thr	Ala	Ala	Leu	Leu														
195										200						205													
GCG	GAG	GCT	TTA	CAC	GCA	TCT	CGT	GTT	GAT	ATC	TGG	ACC	GAC	GTC	CCG	672													
Ala	Glu	Ala	Leu	His	Ala	Ser	Arg	Val	Asp	Ile	Trp	Thr	Asp	Val	Pro														
210										215						220													
GGC	ATC	TAC	ACC	ACC	GAT	CCA	CGC	GTA	GTT	TCC	GCA	GCA	AAA	CGC	ATT	720													
Gly	Ile	Tyr	Thr	Thr	Asp	Pro	Arg	Val	Val	Ser	Ala	Ala	Lys	Arg	Ile														
225										230						235													
GAT	GAA	ATC	GCG	TTT	GCC	GAA	GCG	GCA	GAG	ATG	GCA	ACT	TTT	GGT	GCA	768													
Asp	Glu	Ile	Ala	Phe	Ala	Glu	Ala	Ala	Glu	Met	Ala	Thr	Phe	Gly	Ala														
245										250						255													
AAA	GTA	CTG	CAT	CCG	GCA	ACG	TTG	CTA	CCC	GCA	GTA	CGC	AGC	GAT	ATC	816													
Lys	Val	Leu	His	Pro	Ala	Thr	Leu	Leu	Pro	Ala	Val	Arg	Ser	Asp	Ile														
260										265						270													
CCG	GTC	TTT	GTC	GGC	TCC	AGC	AAA	GAC	CCA	CGC	GCA	GGT	GGT	ACG	CTG	864													
Pro	Val	Phe	Val	Gly	Ser	Ser	Lys	Asp	Pro	Arg	Ala	Gly	Gly	Thr	Leu														
275										280						285													
GTG	TGC	AAT	AAA	ACT	GAA	AAT	CCG	CCG	CTG	TTC	CGC	GCT	CTG	GCG	CTT	912													
Val	Cys	Asn	Lys	Thr	Glu	Asn	Pro	Pro	Leu	Phe	Arg	Ala	Leu	Ala	Leu														
290										295						300													
CGT	CGC	AAT	CAG	ACT	CTG	CTC	ACT	TTG	CAC	AGC	CTG	AAT	ATG	CTG	CAT	960													
Arg	Arg	Asn	Gln	Thr	Leu	Leu	Thr	Leu	His	Ser	Leu	Asn	Met	Leu	His														
305										310						315													
TCT	CGC	GGT	TTC	CTC	GCG	GAA	GTT	TTC	GGC	ATC	CTC	GCG	CGG	CAT	AAT	1008													
Ser	Arg	Gly	Phe	Leu	Ala	Glu	Val	Phe	Gly	Ile	Leu	Ala	Arg	His	Asn														
325										330						335													
ATT	TCG	GTA	GAC	TTA	ATC	ACC	ACG	TCA	GAA	GTG	AGC	GTG	GCA	TTA	ACC	1056													
Ile	Ser	Val	Asp	Leu	Ile	Thr	Thr	Ser	Glu	Val	Ser	Val	Ala	Leu	Thr														
340										345						350													
CTT	GAT	ACC	ACC	GGT	TCA	ACC	TCC	ACT	GGC	GAT	ACG	TTG	CTG	ACG	CAA	1104													
Leu	Asp	Thr	Thr	Gly	Ser	Thr	Ser	Thr	Gly	Asp	Thr	Leu	Leu	Thr	Gln														
355										360						365													
TCT	CTG	CTG	ATG	GAG	CTT	TCC	GCA	CTG	TGT	CGG	GTG	GAG	GTG	GAA	GAA	1152													
Ser	Leu	Leu	Met	Glu	Leu	Ser	Ala	Leu	Cys	Arg	Val	Glu	Val	Glu	Glu														
370										375						380													
GGT	CTG	GCG	CTG	GTC	GCG	TTG	ATT	GGC	AAT	GAC	CTG	TCA	AAA	GCC	TGC	1200													
Gly	Leu	Ala	Leu	Val	Ala	Leu	Ile	Gly	Asn	Asp	Leu	Ser	Lys	Ala	Cys														
385										390						395													
																400													



(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GATATCGAAT TCTCATTATA GAACTCCAGC TTTTTC

37

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 917 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 3..911

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CC ATG GCT ACA GGT TTA ACA GCT AAG ACC GGA GTA GAG CAC TTC GGC	47
Met Ala Thr Gly Leu Thr Ala Lys Thr Gly Val Glu His Phe Gly	
1 5 10 15	
ACC GTT GGA GTA GCA ATG GTT ACT CCA TTC ACG GAA TCC GGA GAC ATC	95
Thr Val Gly Val Ala Met Val Thr Pro Phe Thr Glu Ser Gly Asp Ile	
20 25 30	
GAT ATC GCT GCT GGC CGC GAA GTC GCG GCT TAT TTG GTT GAT AAG GGC	143
Asp Ile Ala Ala Gly Arg Glu Val Ala Ala Tyr Leu Val Asp Lys Gly	
35 40 45	
TTG GAT TCT TTG GTT CTC GCG GGC ACC ACT GGT GAA TCC CCA ACG ACA	191
Leu Asp Ser Leu Val Leu Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr	
50 55 60	
ACC GCC GCT GAA AAA CTA GAA CTG CTC AAG GCC GTT CGT GAG GAA GTT	239
Thr Ala Ala Glu Lys Leu Glu Leu Leu Lys Ala Val Arg Glu Glu Val	
65 70 75	
GGG GAT CGG GCG AAG CTC ATC GCC GGT GTC GGA ACC AAC AAC ACG CGG	287
Gly Asp Arg Ala Lys Leu Ile Ala Gly Val Gly Thr Asn Asn Thr Arg	
80 85 90 95	
ACA TCT GTG GAA CTT GCG GAA GCT GCT GCT TCT GCT GGC GCA GAC GGC	335
Thr Ser Val Glu Leu Ala Glu Ala Ala Ser Ala Gly Ala Asp Gly	
100 105 110	

CTT TTA GTT GTA ACT CCT TAT TAC TCC AAG CCG AGC CAA GAG GGA TTG	383
Leu Leu Val Val Thr Pro Tyr Tyr Ser Lys Pro Ser Gln Glu Gly Leu	
115 120 125	
CTG GCG CAC TTC GGT GCA ATT GCT GCA GCA ACA GAG GTT CCA ATT TGT	431
Leu Ala His Phe Gly Ala Ile Ala Ala Thr Glu Val Pro Ile Cys	
130 135 140	
CTC TAT GAC ATT CCT GGT CGG TCA GGT ATT CCA ATT GAG TCT GAT ACC	479
Leu Tyr Asp Ile Pro Gly Arg Ser Gly Ile Pro Ile Glu Ser Asp Thr	
145 150 155	
ATG AGA CGC CTG AGT GAA TTA CCT ACG ATT TTG GCG GTC AAG GAC GCC	527
Met Arg Arg Leu Ser Glu Leu Pro Thr Ile Leu Ala Val Lys Asp Ala	
160 165 170 175	
AAG GGT GAC CTC GTT GCA GCC ACG TCA TTG ATC AAA GAA ACG GGA CTT	575
Lys Gly Asp Leu Val Ala Ala Thr Ser Leu Ile Lys Glu Thr Gly Leu	
180 185 190	
GCC TGG TAT TCA GGC GAT GAC CCA CTA AAC CTT GTT TGG CTT GCT TTG	623
Ala Trp Tyr Ser Gly Asp Asp Pro Leu Asn Leu Val Trp Leu Ala Leu	
195 200 205	
GGC GGA TCA GGT TTC ATT TCC GTA ATT GGA CAT GCA GCC CCC ACA GCA	671
Gly Gly Ser Gly Phe Ile Ser Val Ile Gly His Ala Ala Pro Thr Ala	
210 215 220	
TTA CGT GAG TTG TAC ACA AGC TTC GAG GAA GGC GAC CTC GTC CGT GCG	719
Leu Arg Glu Leu Tyr Thr Ser Phe Glu Glu Gly Asp Leu Val Arg Ala	
225 230 235	
CGG GAA ATC AAC GCC AAA CTA TCA CCG CTG GTA GCT GCC CAA GGT CGC	767
Arg Glu Ile Asn Ala Lys Leu Ser Pro Leu Val Ala Ala Gln Gly Arg	
240 245 250 255	
TTG GGT GGA GTC AGC TTG GCA AAA GCT GCT CTG CGT CTG CAG GGC ATC	815
Leu Gly Gly Val Ser Leu Ala Lys Ala Ala Leu Arg Leu Gln Gly Ile	
260 265 270	
AAC GTA GGA GAT CCT CGA CTT CCA ATT ATG GCT CCA AAT GAG CAG GAA	863
Asn Val Gly Asp Pro Arg Leu Pro Ile Met Ala Pro Asn Glu Gln Glu	
275 280 285	
CTT GAG GCT CTC CGA GAA GAC ATG AAA AAA GCT GGA GTT CTA TAA TGAGAATTC	918
Leu Glu Ala Leu Arg Glu Asp Met Lys Lys Ala Gly Val Leu *	
290 295 300	

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTTCCCGTGA CCATGGGCCA TC

22

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 75 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CATGGCTGGC TTCCCCACGA GGAAGACCAA CAATGACATT ACCTCCATTG CTAGCAACGG 60

TGGAAGAGTA CAATG 75

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 75 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CATGCATTGT ACTCTTCCAC CGTTGCTAGC AATGGAGGTA ATGTCATTGT TGGTCTTCCT 60

CGTGGGGAAG CCAGC 75

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 90 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CATGGCTTCC TCAATGATCT CCTCCCCAGC TGTTACCACC GTCAACCGTG CCGGTGCCGG 60

CATGGTTGCT CCATTCACCG GCCTCAAAAG 90

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 90 base pairs
  - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CATGCTTTTG AGGCCGGTGA ATGGAGCAAC CATGCCGGCA CCGGCACGGT TGACGGTGGT 60

AACAGCTGGG GAGGAGATCA TTGAGGAAGC 90

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCGTTTGCT GTAATAGGTA CCA 23

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGCTTGGTAC CTATTACAGC AAACCGGCAT G 31

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCTTCCTCAA TGATCTCCTC CCCAGCT 27

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid



(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CATTGTACTC TTCCACCGTT GCTAGCAA

28

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1..20  
(D) OTHER INFORMATION: /product= "synthetic  
oligonucleotide"  
/standard\_name= "SM  
70"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CTGACTCGCT GCGCTCGGTC

20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1..24  
(D) OTHER INFORMATION: /product= "synthetic  
oligonucleotide"  
/standard\_name= "SM  
71"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TATTTTCTCC TTACGCATCT GTGC

24

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /product= "synthetic  
oligonucleotide"  
/standard\_name= "SM  
78"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTCATCGATA GGCGACCACA CCCGTCC

27

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /product= "synthetic  
oligonucleotide"  
/standard\_name= "SM  
79"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AATATCGATG CCACGATGCG TCCGGCG

27

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..55
- (D) OTHER INFORMATION: /product= "synthetic  
oligonucleotide"  
/standard\_name= "SM  
81"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CATGGAGGAG AAGATGAAGG CGATGGAAGA GAAGATGAAG GCGTGATAGG TACCG 55

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..55
- (D) OTHER INFORMATION: /product= "synthetic  
oligonucleotide"  
/standard\_name= "SM  
80"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AATTCGGTAC CTATCAGGCC TTCATCTTCT CTTCCATCGC CTTTCATCTTC TCCTC 55

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..14
- (D) OTHER INFORMATION: /label= name  
/note= "base gene  
[(SSP5)2]"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala  
1 5 10

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1..21  
 (D) OTHER INFORMATION: /product=  
                               "synthetic  
                               oligonucleotide"  
                               /standard\_name= "SM  
                               84"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GATGGAGGAG AAGATGAAGG C 21

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1..21  
 (D) OTHER INFORMATION: /product= "synthetic  
                               oligonucleotide"  
                               /standard\_name= "SM  
                               85"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATCGCCTTCA TCTTCTCCTC C 21

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1..21  
 (D) OTHER INFORMATION: /product= "synthetic  
                               oligonucleotide"  
                               /standard\_name= "SM  
                               82"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GATGGAGGAG AAGCTGAAGG C 21

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /product= "synthetic  
oligonucleotide"  
/standard\_name= "SM  
83"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATCGCCTTCA GCTTCTCCTC C

21

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Glu Glu Lys Leu Lys Ala

1

5

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Glu Glu Lys Met Lys Ala

1

5

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: E. coli

(G) CELL TYPE: DH5 alpha

(vii) IMMEDIATE SOURCE:

(B) CLONE: C15

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..151

(D) OTHER INFORMATION: /function= "synthetic  
storage protein"  
/product= "protein"  
/gene= "ssp"  
/standard\_name=  
"5.7.7.7.7.7.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG 46  
Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met  
1 5 10 15  
GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG 94  
Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu  
20 25 30  
AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAA GAG AAG ATG 142  
Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met  
35 40 45  
AAG GCG TGATAGGTAC CG 160  
Lys Ala  
50

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu  
1 5 10 15  
Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys  
20 25 30

Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met Lys  
 35 40 45

Ala

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: E. coli
- (G) CELL TYPE: DH5 alpha

(vii) IMMEDIATE SOURCE:

- (B) CLONE: C20

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..151
- (D) OTHER INFORMATION: /function= "synthetic  
 storage protein"  
 /product= "protein"  
 /gene= "ssp"  
 /standard\_name=  
 "5.7.7.7.7.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG	46
Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met	
1 5 10 15	
GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG	94
Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu	
20 25 30	
AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAA GAG AAG ATG	142
Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met	
35 40 45	
AAG GCG TGATAGGTAC CG	160
Lys Ala	
50	

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu  
1 5 10 15  
Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys  
20 25 30  
Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met Lys  
35 40 45

Ala

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: E. coli
- (G) CELL TYPE: DH5 alpha

(vii) IMMEDIATE SOURCE:

- (B) CLONE: C30

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..130
- (D) OTHER INFORMATION: /function= "synthetic  
storage protein"  
/product= "protein"  
/gene= "ssp"  
/standard\_name=  
"5.7.7.7.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG 46  
Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met  
1 5 10 15  
GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG 94  
Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu  
20 25 30  
AAG CTG AAG GCG ATG GAA GAG AAG ATG AAG GCG TGATAGGTAC CG 139  
Lys Leu Lys Ala Met Glu Glu Lys Met Lys Ala  
35 40



(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu  
1 5 10 15  
Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys  
20 25 30  
Leu Lys Ala Met Glu Glu Lys Met Lys Ala  
35 40

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: E. coli
- (G) CELL TYPE: DH5 alpha

(vii) IMMEDIATE SOURCE:

- (B) CLONE: D16

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..88
- (D) OTHER INFORMATION: /function= "synthetic  
storage protein"  
/product= "protein"  
/gene= "ssp"  
/standard\_name=  
"5.5.5.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG GCG ATG 46  
Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met  
1 5 10 15  
GAG GAG AAG ATG AAG GCG ATG GAA GAG AAG ATG AAG GCG TGATAGGTAC 95  
Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala  
20 25

CG

97

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

```
Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu
 1             5             10             15
Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala
 20             25
```

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: E. coli
- (G) CELL TYPE: DH5 alpha

(vii) IMMEDIATE SOURCE:

- (B) CLONE: D20

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..109
- (D) OTHER INFORMATION: /function= "synthetic  
storage protein"  
/product= "protein"  
/gene= "ssp"  
/standard\_name=  
"5.5.5.5.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

```
C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG GCG ATG      46
  Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met
    1             5             10             15

GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG GCG ATG GAA GAG    94
Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu Glu
    20             25             30

AAG ATG AAG GCG TGATAGGTAC CG                                     118
Lys Met Lys Ala
    35
```

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu  
1 5 10 15  
Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys  
20 25 30  
Met Lys Ala  
35

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: E. coli
- (G) CELL TYPE: DH5 alpha

(vii) IMMEDIATE SOURCE:

- (B) CLONE: D33

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..88
- (D) OTHER INFORMATION: /function= "synthetic  
storage protein"  
/product= "protein"  
/gene= "ssp"  
/standard\_name=  
"5.5.5.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG GCG ATG 46  
Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met  
1 5 10 15  
GAG GAG AAG ATG AAG GCG ATG GAA GAG AAG ATG AAG GCG TGATAGGTAC 95  
Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala  
20 25

## (2) INFORMATION FOR SEQ ID NO:40:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu  
 1 5 10 15  
 Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala  
 20 25

## (2) INFORMATION FOR SEQ ID NO:41:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /product= "synthetic  
 oligonucleotide"  
 /standard\_name= "SM  
 86"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GATGGAGGAG AAGCTGAAGA A 21

## (2) INFORMATION FOR SEQ ID NO:42:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /product= "synthetic  
 oligonucleotide"  
 /standard\_name= "SM  
 87"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ATCTTCTTCA GCTTCTCCTC C

21

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /product= "synthetic  
oligonucleotide"  
/standard\_name= "SM  
88"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GATGGAGGAG AAGCTGAAGT G

21

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /product= "synthetic  
oligonucleotide"  
/standard\_name= "SM  
89"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ATCCACTTCA GCTTCTCCTC C

21

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1..21  
 (D) OTHER INFORMATION: /product= "synthetic  
 oligonucleotide"  
 /standard\_name= "SM  
 90"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GATGGAGGAG AAGATGAAGA A

21

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1..21  
 (D) OTHER INFORMATION: /product= "synthetic  
 oligonucleotide"  
 /standard\_name= "SM  
 91"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ATCTTCTTCA TCTTCTCCTC C

21

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1..21  
 (D) OTHER INFORMATION: /product= "synthetic  
 oligonucleotide"  
 /standard\_name= "SM  
 92"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GATGGAGGAG AAGATGAAGT G

21

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /product= "synthetic  
oligonucleotide"  
/standard\_name= "SM  
93"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

ATCCACTTCA TCTTCTCCTC C

21

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Met Glu Glu Lys Leu Lys Lys

1

5

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met Glu Glu Lys Leu Lys Trp

1

5

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid

10023066.1201

- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met Glu Glu Lys Met Lys Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 7 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met Glu Glu Lys Met Lys Trp  
1 5

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 160 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
  - (B) STRAIN: E. coli
  - (G) CELL TYPE: DH5 alpha

- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: 82-4

- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 2..151
  - (D) OTHER INFORMATION: /function= "synthetic  
storage protein  
/product= "protein"  
/gene= "ssp"  
/standard name=  
"7.7.7.7.7.7.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

C ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG 46  
Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met  
1 5 10 15



GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG 94  
 Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu  
                     20                    25                    30

AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAA GAG AAG ATG 142  
 Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met  
                     35                    40                    45

AAG GCG TGATAGGTAC CG 160  
 Lys Ala  
                     50

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 49 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu  
   1                    5                    10                    15

Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys  
                     20                    25                    30

Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met Lys  
                     35                    40                    45

Ala

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 97 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (B) STRAIN: E. coli  
 (G) CELL TYPE: DH5 alpha

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: 84-H3

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 2..88  
 (D) OTHER INFORMATION: /function= "synthetic  
   storage protein  
   /product= "protein"

/gene= "ssp"  
 /standard\_name=  
 "5.5.5.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG GCG ATG 46  
 Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met  
 1 5 10 15  
 GAG GAG AAG ATG AAG GCG ATG GAA GAG AAG ATG AAG GCG TGATAGGTAC 95  
 Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala  
 20 25  
 CG 97

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu  
 1 5 10 15  
 Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala  
 20 25

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: E. coli
- (G) CELL TYPE: DH5 alpha

(vii) IMMEDIATE SOURCE:

- (B) CLONE: 86-H23

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..88
- (D) OTHER INFORMATION: /function= "synthetic  
 storage protein  
 /product= "protein"  
 /gene= "ssp"

/standard\_name=  
"5.8.8.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG CTG AAG AAG ATG 46  
Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Lys Met  
1 5 10 15

GAG GAG AAG CTG AAG AAG ATG GAA GAG AAG ATG AAG GCG TGATAGGTAC 95  
Glu Glu Lys Leu Lys Lys Met Glu Glu Lys Met Lys Ala  
20 25

CG 97

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Lys Met Glu  
1 5 10 15

Glu Lys Leu Lys Lys Met Glu Glu Lys Met Lys Ala  
20 25

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: E. coli
- (G) CELL TYPE: DH5 alpha

(vii) IMMEDIATE SOURCE:

- (B) CLONE: 88-2

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..103
- (D) OTHER INFORMATION: /function= "synthetic  
storage protein  
/product= "protein"  
/gene= "ssp"  
/standard\_name=  
"5.9.9.9.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

C ATG GAG GAG AAG ATG AAG GCG AAG AAG CTG AAG TGG ATG GAG GAG 46  
Met Glu Glu Lys Met Lys Ala Lys Lys Leu Lys Trp Met Glu Glu  
1 5 10 15  
AAG CTG AAG TGG ATG GAG GAG AAG CTG AAG TGG ATG GAA GAG AAG ATG 94  
Lys Leu Lys Trp Met Glu Glu Lys Leu Lys Trp Met Glu Glu Lys Met  
20 25 30  
AAG GCG TGATAGGTAC CG 112  
Lys Ala

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Met Glu Glu Lys Met Lys Ala Lys Lys Leu Lys Trp Met Glu Glu Lys  
1 5 10 15  
Leu Lys Trp Met Glu Glu Lys Leu Lys Trp Met Glu Glu Lys Met Lys  
20 25 30  
Ala

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: E. coli
- (G) CELL TYPE: DH5 alpha

(vii) IMMEDIATE SOURCE:

- (B) CLONE: 90-H8

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..109
- (D) OTHER INFORMATION: /function= "synthetic  
storage protein  
/product= "protein"  
/gene= "ssp"

/standard\_name=  
"5.10.10.10.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG AAG ATG 46  
Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Lys Met  
1 5 10 15  
GAG GAG AAG ATG AAG AAG ATG GAG GAG AAG ATG AAG AAG ATG GAA GAG 94  
Glu Glu Lys Met Lys Lys Met Glu Glu Lys Met Lys Lys Met Glu Glu  
20 25 30  
AAG ATG AAG GCG TGATAGGTAC CG 118  
Lys Met Lys Ala  
35

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Lys Met Glu  
1 5 10 15  
Glu Lys Met Lys Lys Met Glu Glu Lys Met Lys Lys Met Glu Glu Lys  
20 25 30  
Met Lys Ala  
35

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: E. coli
- (G) CELL TYPE: DH5 alpha

(vii) IMMEDIATE SOURCE:

- (B) CLONE: 92-2

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..88

(D) OTHER INFORMATION: /function= "synthetic  
storage protein  
/product= "protein"  
/gene= "ssp"  
/standard\_name=  
"5.11.11.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG TGG ATG 46  
Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Trp Met  
1 5 10 15  
GAG GAG AAG ATG AAG TGG ATG GAA GAG AAG ATG AAG GCG TGATAGGTAC 95  
Glu Glu Lys Met Lys Trp Met Glu Glu Lys Met Lys Ala  
20 25  
CG 97

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Trp Met Glu  
1 5 10 15  
Glu Lys Met Lys Trp Met Glu Glu Lys Met Lys Ala  
20 25

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 84 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1..84  
(D) OTHER INFORMATION: /product= "synthetic  
oligonucleotide"  
/standard\_name= "SM  
96"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GATGGAGGAA AAGATGAAGG CGATGGAGGA GAAAATGAAA GCTATGGAGG AAAAGATGAA 60

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: DNA (genomic)

```
(A)  NAME/KEY:  misc_feature
(B)  LOCATION:  1..84
(D)  OTHER INFORMATION:  /product= "synthetic
                           oligonucleotide"
                           /standard_name= "SM
                           97"
```

ATCGCCTTCA TTTTCTCCTC CATCGCTTTC ATCTTTTCCT CCATAGCTTT CATTTTCTCC 60  
TCCATCGCCT TCACTTTTTC CTCC 84

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: protein

```
(A)  NAME/KEY:  Protein
(B)  LOCATION:  1..28
(D)  OTHER INFORMATION:  /label= name
                           /note= "(SSP 5)4"
```

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu  
1 5 10 15

Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala  
20 25

(i) SEQUENCE CHARACTERISTICS:

- 147

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: /product= "synthetic  
oligonucleotide"  
/standard\_name= "SM  
98"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GATGGAGGAA AAGCTGAAAG CGATGGAGGA GAAACTCAAG GCTATGGAAG AAAAGCTTAA 60  
AGCGATGGAG GAGAAACTGA AGGC 84

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: /product= "synthetic  
oligonucleotide"  
/standard\_name= "SM  
99"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

ATCGCCTTCA GTTTCCTCCTC CTACGCTTTA AGCTTTTCTT CCATAGCCTT GAGTTTCTCC 60  
TCCATCGCTT TCAGCTTTTC CTCC 84

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /label= name  
/note= "(SSP 7)4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:



Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu  
 1 5 10 15  
 Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala  
 20 25

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 84 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 1..84
  - (D) OTHER INFORMATION: /product= "synthetic  
 oligonucleotide"  
 /standard\_name= "SM  
 100"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GATGGAGGAA AAGCTTAAGA AGATGGAAGA AAAGCTGAAA TGGATGGAGG AGAAACTCAA 60  
 AAAGATGGAG GAAAAGCTTA AATG 84

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 84 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 1..84
  - (D) OTHER INFORMATION: /product= "synthetic  
 oligonucleotide"  
 /standard\_name= "SM  
 101"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

ATCCATTAA GCTTTTCCTC CTACTTTTGT AGTTTCTCCT CCATCCATTT CAGCTTTTCT 60  
 TCCATCTTCT TAAGCTTTTC CTCC 84

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

```

Met Glu Glu Lys Leu Lys Lys Met Glu Glu Lys Leu Lys Trp Met Glu
1           5           10           15

Glu Lys Leu Lys Lys Met Glu Glu Lys Leu Lys Trp
20           25

```

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: E. coli
- (G) CELL TYPE: DH5 alpha

(vii) IMMEDIATE SOURCE:

- (B) CLONE: 2-9

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..235
- (D) OTHER INFORMATION: /function= "synthetic  
storage protein  
/product= "protein"  
/gene= "ssp"  
/standard\_name=  
"7.7.7.7.7.7.8.9.8.9.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

```

C ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG      46
Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met
1           5           10           15

GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG      94
Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu
20           25           30

AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAG GAA AAG CTT     142
Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu
35           40           45

AAG AAG ATG GAA GAA AAG CTG AAA TGG ATG GAG GAG AAA CTC AAA AAG     190
Lys Lys Met Glu Glu Lys Leu Lys Trp Met Glu Glu Lys Leu Lys Lys
50           55           60

```

ATG GAG GAA AAG CTT AAA TGG ATG GAA GAG AAG ATG AAG GCG TGATAGGTAC 242  
 Met Glu Glu Lys Leu Lys Trp Met Glu Glu Lys Met Lys Ala  
           65                              70                              75

C

243

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu  
   1                              5                              10                              15  
 Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys  
                               20                              25                              30  
 Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys  
                               35                              40                              45  
 Lys Met Glu Glu Lys Leu Lys Trp Met Glu Glu Lys Leu Lys Lys Met  
                               50                              55                              60  
 Glu Glu Lys Leu Lys Trp Met Glu Glu Lys Met Lys Ala  
   65                              70                              75

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: E. coli
- (G) CELL TYPE: DH5 alpha

(vii) IMMEDIATE SOURCE:

- (B) CLONE: 5-1

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..172
- (D) OTHER INFORMATION: /function= "synthetic  
   storage protein  
   /product= "protein"  
   /gene= "ssp"

/standard\_name=  
"5.5.5.7.7.7.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG GCG ATG 46  
Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met  
1 5 10 15  
GAG GAG AAG ATG AAG GCG ATG GAG GAA AAG CTG AAA GCG ATG GAG GAG 94  
Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu  
20 25 30  
AAA CTC AAG GCT ATG GAA GAA AAG CTT AAA GCG ATG GAG GAG AAA CTG 142  
Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu  
35 40 45  
AAG GCC ATG GAA GAG AAG ATG AAG GCG TGATAG 179  
Lys Ala Met Glu Glu Lys Met Lys Ala  
50 55

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 56 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu  
1 5 10 15  
Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys  
20 25 30  
Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys  
35 40 45  
Ala Met Glu Glu Lys Met Lys Ala  
50 55

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 187 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: E. coli  
(G) CELL TYPE: DH5 alpha

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..173
- (D) OTHER INFORMATION: /function= "synthetic  
storage protein  
/product= "protein"  
/gene= "ssp"  
/standard\_name=  
"SSP-3-5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CC ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG 47  
Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met  
1 5 10 15

GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG 95  
Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu  
20 25 30

AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAG GAA AAG ATG 143  
Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met  
35 40 45

AAG GCG ATG GAA GAG AAG ATG AAG GCG TGATAGGTAC CGAATTC 187  
Lys Ala Met Glu Glu Lys Met Lys Ala  
50 55

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu  
1 5 10 15

Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys  
20 25 30

Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met Lys  
35 40 45

Ala Met Glu Glu Lys Met Lys Ala  
50 55

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10023036-24701

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..61
- (D) OTHER INFORMATION: /product= "synthetic  
oligonucleotide"  
/standard\_name= "SM  
107"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

CATGGAGGAG AAGATGAAAA AGCTCGAAGA GAAGATGAAG GTCATGAAGT GATAGGTACC 60

G

61

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..61
- (D) OTHER INFORMATION: /product= "synthetic  
ligonucleotide"  
/standard\_name= "SM  
106"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

AATTCGGTAC CTATCACTTC ATGACCTTCA TCTTCTCTTC GAGCTTTTTC ATCTTCTCCT 60

C

61

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /label= name  
/note= "pSK34 base  
gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Met Glu Glu Lys Met Lys Lys Leu Glu Glu Lys Met Lys Val Met Lys  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..63
- (D) OTHER INFORMATION: /product= "synthetic  
oligonucleotide"  
/standard\_name= "SM  
110"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GCTGGAAGAA AAGATGAAGG CTATGGAGGA CAAGATGAAA TGGCTTGAGG AAAAGATGAA 60  
GAA 63

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..63
- (D) OTHER INFORMATION: /product= "synthetic  
oligonucleotide"  
/standard\_name= "SM  
111"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

AGCTTCTTCA TCTTTTCCTC AAGCCATTTT ATCTTGTCCT CCATAGCCTT CATCTTTTCT 60  
TCC 63

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Met Glu Glu Lys Met Lys Lys Leu Glu Glu Lys Met Lys Ala Met Glu  
1 5 10 15  
Asp Lys Met Lys Trp Leu Glu Glu Lys Met Lys Lys Leu Glu Glu Lys  
20 25 30  
Met Lys Val Met Lys  
35

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Met Glu Glu Lys Met Lys Lys Leu Glu Glu Lys Met Lys Ala Met Glu  
1 5 10 15  
Asp Lys Met Lys Trp Leu Glu Glu Lys Met Lys Lys Leu Glu Glu Lys  
20 25 30  
Met Lys Val Met Lys  
35

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..62
- (D) OTHER INFORMATION: /product= "synthetic  
oligonucleotide"  
/standard\_name= "SM  
112"



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GCTCGAAGAA AGATGAAGGC AATGGAAGAC AAAATGAAGT GGCTTGAGGA GAAAATGAAG 60

AA

62

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..62
- (D) OTHER INFORMATION: /product= "synthetic  
oligonucleotide"  
/standard\_name= "SM  
113"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

AGCTTCTTCA TTTTCTCCTC AAGCCACTTC ATTTTGTCTT CCATTGCCTT CATCTTTCTT 60

CG

62

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Met Glu Glu Lys Met Lys Lys Leu Lys Glu Glu Met Ala Lys Met Lys  
1 5 10 15

Asp Glu Met Trp Lys Leu Lys Glu Glu Met Lys Lys Leu Glu Glu Lys  
20 25 30

Met Lys Val Met Lys  
35

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..63
- (D) OTHER INFORMATION: /product= "synthetic  
oligonucleotide"  
/standard\_name= "SM  
114"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GCTCAAGGAG GAAATGGCTA AGATGAAAGA CGAAATCTGG AAAGTAAAG AGGAAATGAA 60  
GAA 63

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..63
- (D) OTHER INFORMATION: /product= "synthetic  
oligonucleotide"  
/standard\_name= "SM  
115"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

AGCTTCTTCA TTTCCTCTTT CAGTTTCCAC ATTTCGTCTT TCATCTTAGC CATTTCTCTC 60  
TTG 63

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Met Glu Glu Lys Met Lys Lys Leu Lys Glu Glu Met Ala Lys Met Lys  
1 5 10 15  
Asp Glu Met Trp Lys Leu Lys Glu Glu Met Lys Lys Leu Glu Glu Lys  
20 25 30  
Met Lys Val Met Glu Glu Lys Met Lys Lys Leu Glu Glu Lys Met Lys

Ala Met Glu Asp Lys Met Lys Trp Leu Glu Glu Lys Met Lys Lys Leu  
 50 55 60

Glu Glu Lys Met Lys Val Met Glu Glu Lys Met Lys Lys Leu Glu Glu  
 65 70 75 80

Lys Met Lys Ala Met Glu Asp Lys Met Lys Trp Leu Glu Glu Lys Met  
 85 90 95

Lys Lys Leu Glu Glu Lys Met Lys Val Met Lys  
 100 105

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 839 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GGATCCCCCG GGCTGCAGGA ATTCTACGTA CCATATAGTA AGACTTTGTA TATAAGACGT 60  
 CACCTCTTAC GTGCATGGTT ATATGTGACA TGTGCAGTGA CGTTGTACCA TATAGTAAGA 120  
 CTTTGTATAT AAGACGTCAC CTCTTACGTG CATGGTTATA TGTGACATGT GCAGTGACGT 180  
 TAACCGCACC CTCCTTCCCG TCGTTTCCCA TCTCTTCCTC CTTTAGAGCT ACCACTATAT 240  
 AAATCAGGGC TCATTTTCTC GTCCTCACA GGCTCATCAG CACCCCGGCA GTGCCACCCC 300  
 GACTCCCTGC ACCTGCCATG GGTACGCTAG CCCGGGAGAT CTGACAAAGC AGCATTAGTC 360  
 CGTTGATCGG TGGAAGACCA CTCGTCAGTG TTGAGTTGAA TGTTTGATCA ATAAAATACG 420  
 GCAATGCTGT AAGGGTTGTT TTTTATGCCA TTGATAATAC ACTGTACTGT TCAGTTGTTG 480  
 AACTCTATTT CTTAGCCATG CCAGTGCTTT TCTTATTTTG AATAACATTA CAGCAAAAAG 540  
 TTGAAAGACA AAAAAANNNN NCCCCGAACA GAGTGCTTTG GGTCCCAAGC TTCTTTAGAC 600  
 TGTGTTCCGC GTTCCCCCTA AATTTCTCCC CTATATCTCA CTCACTTGTC ACATCAGCGT 660  
 TCTCTTTCCC CTATATCTCC ACGCTCTACA GCAGTTCCAC CTATATCAAA CCTCTATACC 720  
 CCACCACAAC AATATTATAT ACTTTCATCT TCACCTAACT CATGTACCTT CCAATTTTTT 780  
 TCTACTAATA ATTATTTACG TGCACAGAAA CTTAGGCAAG GGAGAGAGAG AGCGGTACC 839

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 43 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CTAGAAGCCT CGGCAACGTC AGCAACGGCG GAAGAATCCG GTG 43

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

CATGCACCGG ATTCTTCCGC CGTTGCTGAC GTTGCCGAGG CTT 43

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GATCCCATGG CGCCCCTTAA GTCCACCGCC AGCCTCCCCG TCGCCCGCCG CTCCT 55

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CTAGAGGAGC GCGGGGCGAC GGGGAGGCTG GCGGTGGACT TAAGGGGCGC CATGG 55

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

CATGGCGCCC ACCGTGATGA TGGCCTCGTC GGCCACCGCC GTCGCTCCGT TCCAGGGGC  
59

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

TTAAGCCCCT GGAACGGAGC GACGGCGGTG GCCGACGAGG CCATCATCAC GGTGGGCGC  
59

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GCGCCCACCG TGATGA

16

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

CACCGGATTC TTCCGC

16

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 372 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

5 GTAAGATTGG TAAAGTCCAG CAAGAAAATG AGATAAAAGA GAAGCCTGAA ATGACGAAAA 60  
AATCAGGTGT TTTGATTCTT GGTGCTGGAC GTGTGTNTCG CCCAGCTGCT GATTTCCTAG 120  
CTTCAGTTAG AACCATTTTCG TCACAGCAAT GGTACAAAAC ATATTTTCGGA GCAGACTCTG 180  
10 AAGAGAAAAC AGATGTTTCAT GTGATTGTCG CGTCTCTGTA TCTTAAGGAT GCCAAAGAGA 240  
CGGTTGAAGG TATTTTCAGAT GTAGAAGCAG TTCGGCTAGA TGTATCTGAT AGTGAAAGTC 300  
15 TCCTTAAGTA TGTTTCTCAG GTTGATGTTG TCCTAAGTTT ATTACCTGCA AGTTGTCATG 360  
CTTGTGTTAG CA 372

(2) INFORMATION FOR SEQ ID NO:103:

20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 323 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

25 GGAAGCACAC TGCAGACTCTT TTGGAATTCTG GGGACATCAA GAATGGACAA ACAACAACCG 60  
CTATGGCCAA GACTGTTGGG ATCCCTGCAG CCATTGGAGC TCTGCTGTTA ATTGAAGACA 120  
30 AGATCAAGAC AAGAGGAGTC TTAAGGCCTC TCGAAGCAGA GGTGTATTTG CCAGCTTTGG 180  
ATATATTGCA AGCATATGGT ATAAAGCTGA TGGAGAAGGC AGAATGATCA AAGAACTCTG 240  
TATATTGTTT CTNTCTATAA CTTGGAGTTG GAGACAAAGC TGAAGGAGNC AGNGCCATTA 300  
35 GACCAGCAAA AAAAGGAGGA GGA 323

(2) INFORMATION FOR SEQ ID NO:104:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 123 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

5 Lys Ile Gly Lys Val Gln Gln Glu Asn Glu Ile Lys Glu Lys Pro Glu  
1 5 10 15  
Met Thr Lys Lys Ser Gly Val Leu Ile Leu Gly Ala Gly Arg Val Xaa  
20 25 30  
10 Arg Pro Ala Ala Asp Phe Leu Ala Ser Val Arg Thr Ile Ser Ser Gln  
35 40 45  
Gln Trp Tyr Lys Thr Tyr Phe Gly Ala Asp Ser Glu Glu Lys Thr Asp  
50 55 60  
15 Val His Val Ile Val Ala Ser Leu Tyr Leu Lys Asp Ala Lys Glu Thr  
65 70 75 80  
Val Glu Gly Ile Ser Asp Val Glu Ala Val Arg Leu Asp Val Ser Asp  
85 90 95  
20 Ser Glu Ser Leu Leu Lys Tyr Val Ser Gln Val Asp Val Val Leu Ser  
100 105 110  
Leu Leu Pro Ala Ser Cys His Ala Cys Cys Ser  
115 120  
25

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 74 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

35 Lys His Thr Ala Thr Leu Leu Glu Phe Gly Asp Ile Lys Asn Gly Gln  
1 5 10 15  
Thr Thr Thr Ala Met Ala Lys Thr Val Gly Ile Pro Ala Ala Ile Gly  
20 25 30  
40 Ala Leu Leu Leu Ile Glu Asp Lys Ile Lys Thr Arg Gly Val Leu Arg  
35 40 45  
Pro Leu Glu Ala Glu Val Tyr Leu Pro Ala Leu Asp Ile Leu Gln Ala  
50 55 60  
45 Tyr Gly Ile Lys Leu Met Glu Lys Ala Glu  
65 70

50 (2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

5

ATTCCCCATG GTTTCGCCGA CGAAT

25

(2) INFORMATION FOR SEQ ID NO:107:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

15

CTCTCGGTAC CTAGTACCTA CTGATCAAC

29